

- (b) VVVVSTTGTGDPPDTARKFVKEI (SEQ ID NO: 53),
- (c) AHLRYGLLGLGDSEYTYFCNGGKIIDKRL (SEQ ID NO: 54),
- (d) LQPRPYSCASSSLFHPGKL (SEQ ID NO: 55),
- (e) FVFNIVEFLSTATT (SEQ ID NO: 56),
- (f) LRKGVCTGWLALLVASV (SEQ ID NO: 57),
- (g) IPIIMVGPGTGLAPFIGFLQHR (SEQ ID NO: 58),
- (h) SFSRDA (SEQ ID NO: 59),
- (i) APAKYVQDNIQLHGQQVARILLQENGHIYVCGDAKNMAKDV  
(SEQ ID NO: 60), or
- (j) KRYLQDIWS (SEQ ID NO: 61).

50-55 (Cancelled)

56. (New) A substantially pure nucleic acid molecule having at least 95% sequence identity to SEQ ID NO: 1 and encoding a mammalian methionine synthase reductase polypeptide, wherein said polypeptide is capable of catalyzing the reductive methylation of methionine synthase-cob(II)alamin to generate methionine synthase-cob(III)alamin-CH<sub>3</sub>.

57. (New) The nucleic acid of claim 56, wherein said nucleic acid molecule has the sequence of SEQ ID NO: 1.

58. (New) The nucleic acid molecule of claim 56, wherein said nucleic acid molecule

encodes a human methionine synthase reductase polypeptide.

59. (New) The nucleic acid molecule of claim 56, wherein said nucleic acid molecule encodes a mammalian methionine synthase reductase polypeptide having at least 20% of the methionine synthase reductase activity of the methionine synthase reductase polypeptide of SEQ ID NO: 2.

60. (New) The nucleic acid molecule of claim 59, wherein said nucleic acid molecule encodes a mammalian methionine synthase reductase polypeptide having at least 55% of the methionine synthase reductase activity of the methionine synthase reductase polypeptide of SEQ ID NO: 2.

61. (New) The nucleic acid molecule of claim 56, wherein said nucleic acid molecule encodes a mammalian methionine synthase reductase polypeptide that comprises a consensus binding site for one or more cofactors selected from the group consisting of FAD, FMN, and NADPH, wherein said binding site comprises any one of SEQ ID NOs: 25 or 52-61.

62. (New) The nucleic acid molecule of claim 56, wherein the polynucleotide sequence of said nucleic acid molecule comprises a mutation or polymorphism present in a naturally-occurring mammalian methionine synthase reductase gene.

63. (New) A substantially pure nucleic acid molecule having at least 95% sequence

identity to SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, or SEQ ID NO: 47 and encoding a mammalian methionine synthase reductase polypeptide that has a reduced ability to catalyze the reductive methylation of methionine synthase-cob(II)alamin to generate methionine synthase-cob(III)alamin-CH<sub>3</sub> relative to the methionine synthase reductase activity of a mammalian methionine synthase reductase polypeptide encoded by SEQ ID NO: 1.

64. (New) The nucleic acid of claim 63, wherein said nucleic acid molecule has the sequence of SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, or SEQ ID NO: 47.

65. (New) The nucleic acid molecule of claim 63, wherein said nucleic acid molecule encodes a human methionine synthase reductase polypeptide.

66. (New) The nucleic acid molecule of claim 63, wherein said nucleic acid molecule encodes a mammalian methionine synthase reductase polypeptide that comprises a consensus binding site for one or more cofactors selected from the group consisting of FAD, FMN, and NADPH, wherein said binding site comprises any one of SEQ ID NOs: 25 or 52-61.

67. (New) The nucleic acid molecule of claim 63, wherein the polynucleotide sequence of said nucleic acid molecule comprises a mutation or polymorphism present in a naturally-occurring mammalian methionine synthase reductase gene.

68. (New) A substantially pure antisense nucleic acid molecule having a polynucleotide

sequence that is completely complementary to at least 18 contiguous nucleotides of a mammalian methionine synthase reductase gene having the polynucleotide sequence of SEQ ID NO: 1, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, or SEQ ID NO: 47.

69. (New) The antisense nucleic acid molecule of claim 68, wherein said antisense nucleic acid molecule comprises a polynucleotide sequence the complete complement of which comprises a consensus binding site for one or more cofactors present in a selected from the group consisting of FAD, FMN, and NADPH, wherein said binding site comprises any one of SEQ ID NOs: 25 or 52-61.

70. (New) The antisense nucleic acid molecule of claim 68, wherein said antisense nucleic acid molecule comprises a polynucleotide sequence the complete complement of which comprises a mutation or polymorphism present in a naturally-occurring mammalian methionine synthase reductase gene.